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PCT09

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/786,926

DATE: 07/27/2001  
 TIME: 19:54:31

ENTERED

Input Set : A:\ES.txt  
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3 <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin  
 5 <120> TITLE OF INVENTION: Human and murine G-protein coupled EDG6 receptor  
 6 (endothelial differentiation gene) and use of same  
 8 <130> FILE REFERENCE: 101195-45  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/786,926  
 11 <141> CURRENT FILING DATE: 2001-03-09  
 13 <150> PRIOR APPLICATION NUMBER: DE 198 43 240.2  
 14 <151> PRIOR FILING DATE: 1998-09-11  
 16 <150> PRIOR APPLICATION NUMBER: DE 198 46 979.9  
 17 <151> PRIOR FILING DATE: 1998-10-13  
 19 <150> PRIOR APPLICATION NUMBER: PCT/DE 99/02871  
 20 <151> PRIOR FILING DATE: 1999-09-10  
 22 <160> NUMBER OF SEQ ID NOS: 4  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 384  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Artificial Sequence  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: Description of Artificial Sequence: human  
 33 G-protein-coupled EDG6 receptor  
 35 <400> SEQUENCE: 1  
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 37 1 5 10 15  
 39 Ala Ala Gly Gly His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser  
 40 20 25 30  
 42 Gly Arg Leu Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala  
 43 35 40 45  
 45 Leu Arg Gly Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn  
 46 50 55 60  
 48 Leu Leu Val Leu Ala Ala Ile Thr Ser His Met Arg Ser Arg Arg Trp  
 49 65 70 75 80  
 51 Val Tyr Tyr Cys Leu Val Asn Ile Thr Leu Ser Asp Leu Leu Thr Gly  
 52 85 90 95  
 54 Ala Ala Tyr Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg  
 55 100 105 110  
 57 Leu Ala Pro Ala Gln Trp Phe Leu Arg Glu Gly Leu Leu Phe Thr Ala  
 58 115 120 125  
 60 Leu Ala Ala Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Glu Arg Phe  
 61 130 135 140  
 63 Ala Thr Met Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser  
 64 145 150 155 160  
 66 Arg Val Tyr Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu  
 67 165 170 175  
 69 Gly Met Leu Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg  
 70 180 185 190  
 72 Cys Ser Ser Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys

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75 Leu Val Ile Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly
76          210          215          220
78 Ala Ile Phe Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro
79 225          230          235          240
81 Ala Ala Arg Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile
82          245          250          255
84 Leu Leu Ala Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Leu
85          260          265          270
87 Ala Asp Val Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly
88          275          280          285
90 Met Asp Trp Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro
91          290          295          300
93 Ile Ile Tyr Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser
94 305          310          315          320
96 Phe Leu Cys Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp
97          325          330          335
99 Cys Leu Ala Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp
100          340          345          350
102 Ser Ser Leu Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser
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119 <223> OTHER INFORMATION: Description of Artificial Sequence: human edg6
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125 ccgagggatg gcggcctggg ggccctgcgg gggctgtcgg tggccgccag ctgcctggtg 180
126 gtgctggaga acttgctggt gctggcggcc atcaccagcc acatgcggtc gcgacgctgg 240
127 gtctactatt gcctggtgaa catcacgctg agtgacctgc tcacgggcgc ggcctacctg 300
128 gccaacgtgc tgetgtcggg ggcgcgcacc ttccgtcttg cgcccgccca gtggttcccta 360
129 cgggagggcc tgetcttcac cgccctggcc gctccacct tcagcctgct cttcactgca 420
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134 ggctctatg gggccatctt ccgcctggtg caggccagcg ggcagaaggc cccacgcccc 720
135 gcggcccgcc gcaaggcccg ccgcctgctg aagacggtgc tgatgatcct gctggccttc 780
136 ctggtgtgct ggggcccact cttcgggctg ctgctggccg acgtcttttg ctccaacctc 840
137 tgggccagag agtacctgcg gggcatggac tggatcctgg ccctggccgt cctcaactcg 900
138 gcggtcaacc ccatcatcta ctcttcgcg agcagggagg tgtgcagagc cgtgctcagc 960
139 ttctctgct gcgggtgtct ccggtgggac atgcgagggc ccggggactg cctggcccg 1020
140 gccgtcgagg ctactccgg agcttcacc accgacagct ctctgaggcc aaggacagc 1080

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141 tttcgcggct cccgctcgct cagctttcgg atgcgggagc ccctgtccag catctccagc 1140
142 gtgcggagca tctga 1155
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146 <211> LENGTH: 1161
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence: murine edg6
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157 gggggctctg aggacggtg agggctaggg atgctgaggg ggccgtcggg ggccgcaggc 180
158 tgcttggtgg tgcggagaa cgccatggtg ctggccgcca tcgccatcta catgcggctc 240
159 cgccgctggg tgtactactg cctgctgaac atcacactga gtgacctgct cacaggcctg 300
160 gcctacgtgg tcaacgtgct gctgtcaggg actcgtacct tccagctgtc accggtgcac 360
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162 ttcacggccg gcgagcgctt cgccaccatg gtgcgggtgg ctgagagtgg ggccaccaag 480
163 accagccgtg tgtatggctg catcggctctg tgcctggctac tggcagctat cctgggcctg 540
164 ctgcccctgc tgggctggaa ctgtgtgtgc gccttccac gctgctccag cctgctgccc 600
165 ctctactoca agggctatgt gctcttttgt gtgggtggtc tcgccctcat cctagtggct 660
166 atcctgagcc tctacggggc catctttaga gtggtccgag ccaatgggca gaagtctcca 720
167 cgtcctcctg cccgccgcaa gtcccgcagg ctactcaaca ccgtgctgat gatcttggtg 780
168 gcctttgtgg tgtgctgggg tcccctgttt ggccgtgtcc tggctgacat ctttggttct 840
169 aatgtctggg cccaggagta cctgctgtgc atggactgga tcctggccct ggccgtgttc 900
170 aactcagcca ttaatcctct catctactcc ttccgcagcc gtgaggtgca gcgcgctgtg 960
171 ctggccttcc tgtgctgcgg ctgtctctgg ctaggctctg gaggtccagg agactgctg 1020
172 acccgatca cggaggccca ctccggtgca tccaccactg acagctccct gaggccagc 1080
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178 <211> LENGTH: 386
179 <212> TYPE: PRT
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182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: murine
184     G-protein-coupled EDG6 receptor
186 <400> SEQUENCE: 4
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188   1             5             10             15
190 Arg Leu Ala Ala Ser Gly His Ser Leu Leu Ile Val Leu His Tyr Asn
191             20             25             30
193 His Ser Gly Arg Leu Ala Ser Arg Gly Gly Ser Glu Asp Gly Gly Gly
194             35             40             45
196 Leu Gly Met Leu Arg Gly Pro Ser Val Ala Ala Gly Cys Leu Val Val
197             50             55             60
199 Leu Glu Asn Ala Met Val Leu Ala Ala Ile Ala Ile Tyr Met Arg Ser
200   65             70             75             80
202 Arg Arg Trp Val Tyr Tyr Cys Leu Leu Asn Ile Thr Leu Ser Asp Leu

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208	Thr	Phe	Gln	Leu	Ser	Pro	Val	His	Trp	Phe	Leu	Arg	Glu	Gly	Leu	Leu
209			115					120					125			
211	Phe	Met	Ala	Leu	Ala	Ala	Ser	Thr	Phe	Ser	Leu	Leu	Phe	Thr	Ala	Gly
212		130						135				140				
214	Glu	Arg	Phe	Ala	Thr	Met	Val	Arg	Val	Ala	Glu	Ser	Gly	Ala	Thr	Lys
215	145					150					155					160
217	Thr	Ser	Arg	Val	Tyr	Gly	Cys	Ile	Gly	Leu	Cys	Trp	Leu	Leu	Ala	Ala
218				165					170						175	
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221				180					185				190			
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224			195					200					205			
226	Phe	Cys	Val	Val	Val	Phe	Ala	Leu	Ile	Leu	Val	Ala	Ile	Leu	Ser	Leu
227		210					215					220				
229	Tyr	Gly	Ala	Ile	Phe	Arg	Val	Val	Arg	Ala	Asn	Gly	Gln	Lys	Ser	Pro
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233				245					250					255		
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236			260						265				270			
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239			275					280				285				
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242		290					295					300				
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245	305					310					315					320
247	Leu	Ala	Phe	Leu	Cys	Cys	Gly	Cys	Leu	Trp	Leu	Gly	Leu	Arg	Gly	Pro
248				325					330				335			
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251			340					345				350				
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257		370				375					380					
259	Ser	Thr														
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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number